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Minimum
Maximum
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No.
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Maximum Match
                                                                                                                                                                                                                                                                                              Database
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                     DB
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 59.55
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61
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length: 2000000000
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1: pir1:*
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4: pir4:*
 Match
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Gapop 10.0 ,
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275
1 GDDDPPKRYEDCRRRCEWDT.....
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                                                                                                                                                                                                                                                                                                                                                                     195891 seqs, 67900655 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version Copyright (c) 1993 - 2000
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first 45 summaries
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ID
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20.5	20.7	20.7	20.7	20.7	20.7	20.9	20.9	21.1	21.1	21.3	21.5	21.5	21.5	21.5	21.5
388	1898	942	493	342	330	527	225	419	338	1085	2165	2150	1339	748	544
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hypothetical prote	trichohyalin - hum		hypothetical prote	brain-specific mem	rifin PFB0040c - m	_	_	hypothetical prote	legumin B (clone p	hypothetical coile	hypothetical prote	sensory transducti	DNA-directed DNA p	disintegrin (EC 3.	disintegrin (EC 3.

ALIGNMENTS

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alpha-globulin type A precursor - upland cotton N;Alternate names: seed storage protein C;Species: Gossyplum hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change C;Accession: S06598 R;Chlan C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                          RESULT
S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-81 <CH2>
C; Comment: This is a seed storage protein.
C; Superfamily: glycinin
C; Keywords: glycoprotein; seed; storage protein
C; Keywords: glycoprotein; seed; storage protein
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
F; 417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-globulin B precursor (clone C72) - upland cotton
N;Alternate names: seed storage protein; vicilin precursor
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30838; S06911
R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A;Reference number: A30838
A;Accession: A30838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S06398
A;Accession: S06911
A;Status: not compared with conceptual translation
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R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III,
Plant Mol. Biol. 9, 533-546, 1987
A; Title: Developmental biochemistry of cottonseed embryogenesis A; Reference number: $506398
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A; Residues: 1-588 < CHL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1;
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Best Local S
Matches 47
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Pred. No. 1.2
0; Mismatches
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.2e-22;
s 0;
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A; Molecule type: DNA
A; Residues: 1-509 <CHL>
C; Superfamily: glycinin
                                                                                                                                                   A; Reference number: S06398
A; Accession: S08059
                                                                                                                                                                                                         R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                          C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S08059
                                                                                                                                                                                                                                                                                                  alpha-globulin type B precursor (tandem 1) - upland cotton (fragment) N; Alternate names: seed storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-566/Product: vicilin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;McHenry, L.; Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nucleotide sequence A;Reference number: S22477; MUID:92288309
A;Accession: S22477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C:Accession: S22477; S22478; S18105; S22050
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>
                                                                                                                                                                                        A; Title: Developmental biochemistry of cottonseed embryogenesis and
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A; Residues: 1-452 < MC2>
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                                                                                                                                 A; Status: not compared with
                                                                                                                                                                                                                                                                                                                                           S08059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references: EMBL: X62626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X62625
A;Accession: S22478
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A; Residues: 1-566 <MCH>
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 Best Local Similarity
                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 45.1%;
Similarity 46.3%;
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36
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Pred. No. 5.8e-08;
 Score
Pred.
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Pred. No. 3e-06;
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 94.5;
No. 0.
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 DB 2
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                   Length 509;
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                 A; Status: preliminary
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Best Local Similarity
Matches 15; Conserv
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A; Residues: 1-810 < YAM>
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A; Molecule type: mRNA
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R;Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, I.
J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a sin A;Reference number: Z22767; MUID:99107919
A;Accession: T44430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G. Biosci. Biotechnol. Biochem. 61, 984-988, 1997
A:Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide A;Reference number: JC5557; MUID:97357433
A:Accession: JC5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
Biochem. Biophys. Res. Commun. 169, 730-736, 1990 A;Title: Sequences of three VSG mRNAs expressed in A:Reference number: A35480; MUID:90290520 A;Accession: A35480
                                                                                         C:Accession: A35480
R;Reddy, L.V.; Hall, T.; Donelson, J.E.
                                                                                                                                       variant surface glycoprotein WRATatA precursor - Trypanosoma C;Species: Trypanosoma brucei rhodesiense C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Comment: This protein is a storage protein whire F;12-33,16-29/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arginine/glutamate-rich 6.5K polypeptide - smooth loofah C;Species: Luffa cyllindrica (smooth loofah) C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text. C;Accession: JC5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1;
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                                                                                                                                                                                                                                                                                                                                                      5 PPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQ
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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984-988, 1997
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Pred. No. 0.
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Pred. No.
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                                             mixed population
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C; Species: Homo sapiens (man)
C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C; Accession: $50830
R; Kawaguchi, Y.; Okamoto, T.; Taniwaki, M.; Alzawa, M.; Inoue, M.; Katayama, S.; Kawaka Nature Genet. 8, 221-228, 1994
A; Title: CAG expansions in a novel gene for Machado-Joseph disease at chromosome 14q32.
A; Reference number: $50830; MUID:95179166
A; Accession: $50830
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:T01D1.6
A; Map position: 2
A; Introns: 25/3; 304/3
C; Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: DNA
A;Residues: 1-411 <BRA>
A;Cross-references: EMBL:U80455; PIDN:AAB37887.1; GSPDB:GN00020; CESP:T01D1.6
A;Experimental source: strain Bristol N2; clone T01D1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T01D1.6 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C:Accession: T29475 R:Bradshaw, H.: Wohldmann, P.
                                                                                                                                                                  A;Molecule type: mRNĀ
A;Residues: 1-360 <KAW>
A;Cross-references: GB:S75313; NID:g833927; PIDN:AAB33571.1; PID:g833928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
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A;Reference number: 220623
A;Accession: T29475
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-471 <RED>
A;Cross-references: GB:M33823; NID:g162487; PID:g162488 C;Superfamily: variant surface glycoprotein C;Keywords: glycoprotein
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                                    EDCRRRCE--WDTRGQKEQQQCEESCKSQYGEKDQQQRHR 47
                  14;
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Pred. No. 5;
11; Mismatches
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Pred. No. 3
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                  C; Genetics:
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A;Gene: tagB
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A;Status: pro-
A;Molecule type: DNA
A;Residues: 1-1905 <SHA>
                                                                                                                                                                        C;Accession: T18267
R;Shaulsky, G; Kuspa, A.; Loomis, W.F.
submitted to the EMBL Data Library, January 1995
A;Description: An MDR transporter/serine protease
                                                                                                                                                                                                                                                                               multidrug resistance protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Larocca, D.; Chao, L.A.; Seto, M.H.; Brunck, T.K. Biochem. Biophys. Res. Commun. 163, 1006-1013, 1989 A;Title: Human T-cell leukemia virus minus strand transcription A;Reference number: A33513; MUID:89391952 A;Accession: A33513
A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein B - human T-cell lymphotropic virus type 1
C;Species: human T-cell lymphotropic virus type 1, HTLV-1
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-189 <TOM> A;Cross-references: GB:AE000532; GB:AE000511; NID:g2313184; PIDN:AAD07179.1; PID:g231 C;Superfamily: heat shock protein grpE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 C;Accession: F64533 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R;Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKeson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467
A;Accession: F64533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: genomic RNA
A; Residues: 1-265 <LAR>
                                                                                            A; Status: preliminary; translated from
                                                                                                                        A; Accession: T18267
                                                                                                                                                    A; Reference number: 218850
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Best Local
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Pred. No. 11;
17; Mismatches
                NID: 9664839; PID: 9664840;
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7.8;
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A;Molecule type: DNA
A;Residues: 1-1819 <ARN>
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C;Accession: A71928
C;Accession: A71928
C;Accession: A71928
C;Accession: A71928
C;Accession: A71928
No.T.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557
A;Accession: A71928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cag island protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A71928
                                                                              В
                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001481; GB:AE001439; NID:g4155005; PIDN:AAD06047.1; PID:g415500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21688 R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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н81536
                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 2
A; Introns: 29/3; 56/3; 98/2; 225/2; 384/3; 419/1; 488/2; 517/3; 637/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T21688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1996 A; Reference number: Z19459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F33A8.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP:F33A8.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone F33A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-897 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity 28.3
Matches 13; Conservative
                                                                          1242 KAYLDCVSR----ARNEKEKQECEKLLTPEARKFLEKQRQQKDK 1281
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                15
                                                                                                   7 KRYEDCRRRCEWDTRGQKEQQQCEESCKSQ---YGEKDQQQRHR 47
                                                                                                                                                                                                                                                          orf13/14
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: Z81525; PIDN: CAB04256.1; GSPDB: GN00020; CESP: F33A8.1
                                                                                                                                                                         22.0%;
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Pred. No.
                                                                                                                                                         9; Mismatches
                                                                                                                                                                         Score 60.5;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.5; D
Pred. No. 35;
15; Mismatches
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60;
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                                                                                                                                                         Indels
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C;Accession: H81536
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke R;Read, T.D.; Brunham, R.C.; Shen, C.; Geboy, R.; Kolonay, J.; McClarty, G.; Salzbe C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein CP0796 [imported] - Chlamydophila pneumoniae (strain AR39) C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000
Search completed: March Job time: 568 sec
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                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CP0796
C;Superfamily: Chlamydophila pneumoniae hypothetical protein CP0796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE002239; GB:AE002161; NID:g7189708; PIDN:AAF38595.1; PID:g718 A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-241 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A81500; MUID:20150255
A;Accession: H81536
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.2
Matches 11; Conservative
                                                                                                                                      51 DEDLRRAYTECQKRFQGDSGLESEVRACREQLRERIQEFETQ
                                                                                                                                                                                               2 DDDPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQ 43
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                       2001, 15:52:44
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Pred. No.
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